

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

- (i) APPLICANT: Brodeur, Bernard R
Martin, Denis
Hamel, Josee
10 Rioux, Clement
- (ii) TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
- 15 (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Montreal
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(E) COUNTRY: Canada
(F) ZIP: H4Z 1E9
- 25 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
35 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/406,362
40 (B) FILING DATE: 17-MAR-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US (PROVIS) 60/001,983
(B) FILING DATE: 04-AUG-1995
- 45 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Leclerc/Dubuc/Prince, Alain/Jean/Gaetan
(C) REFERENCE/DOCKET NUMBER: BIOVAC-1 PCT
- (ix) TELECOMMUNICATION INFORMATION:
50 (A) TELEPHONE: 514-397-7400
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55 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
60 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: 608B

10 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 143..667

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 15 (B) LOCATION: 143..199

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 20 (B) LOCATION: 200..667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

25 TCGGCAAGGC AGCCGGATAC CGCTACGTAT CTTGAAGTAT TGAAAATATT ACGATGCAAA 60
 AAAGAAAATT TAAGTATAAT ACAGCAGGAT TCTTTAACGG ATTCTTAACA ATTTTCTAA 120
 CTGACCATAA AGGAACCAAA AT ATG AAA AAA GCA CTT GCC ACA CTG ATT GCC 172
 Met Lys Lys Ala Leu Ala Thr Leu Ile Ala
 30 -19 -15 -10

CTC GCT CTC CCG GCC GCC GCA CTG GCG GAA GGC GCA TCC GGC TTT TAC 220
 Leu Ala Leu Pro Ala Ala Leu Ala Gly Gly Ala Ser Gly Phe Tyr
 -5 1 5

35 GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA GGT TCT 268
 Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Leu Gly Ser
 10 15 20

40 GCC AAA GGC TTC AGC CCG CGC ATC TCC GCA GGC TAC CGC ATC AAC GAC 316
 Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp
 25 30 35

45 CTC CGC TTC GCC GTC GAT TAC ACG CGC TAC AAA AAC TAT AAA GCC CCA 364
 Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro
 40 45 50 55

TCC ACC GAT TTC AAA CTT TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC 412
 Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp
 50 60 65 70

TTC GAC ACC CAA TCG CCC GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC 460
 Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser
 75 80 85

55 CTC AAC CGC GCC TCC GTC GAC TTG GGC GGC AGC GAC AGC TTC AGC CAA 508
 Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln
 90 95 100

60 ACC TCC ATC GGC CTC GGC GTA TTG ACG GGC GTA AGC TAT GCC GTT ACC 556
 Thr Ser Ile Gly Leu Gly Val Leu Thr Gly Val Ser Tyr Ala Val Thr
 105 110 115

CCG AAT GTC GAT TTG GAT GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA 604
 Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys
 120 125 130 135

5 GTC AAC ACT GTC AAA AAC GTC CGT TCC GGC GAA CTG TCC GTC GGC GTG 652
 Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Val Gly Val
 140 145 150

10 CGC GTC AAA TTC TGATATGCGC CTTATTCTGC AAACCGCCGA GCCTTCGGCG 704
 Arg Val Lys Phe
 155

GTTTTGT TTTT CTGCCACCGC AACTACACAA GCCGGCGGTT TTGTACGATA ATCCCGAATG 764

15 CTGCGGCTTC TGCCGCCCTA TTTTGTGAGG AATCCGAAT GTCCAAAACC ATCATCCACA
 824
 ACA 830

20 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids.
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala
 -19 -15 -10 -5

35 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
 1 5 10

His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
 15 20 25

40 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
 30 35 40 45

Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu
 50 55 60

45 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
 65 70 75

50 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
 80 85 90

Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Ile Gly Leu Gly
 95 100 105

55 Val Leu Thr Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
 110 115 120 125

Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
 130 135 140

60 Val Arg Ser Gly Glu Leu Ser Val Gly Val Arg Val Lys Phe
 145 150 155

(2) INFORMATION FOR SEQ ID NO:3:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 710 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Neisseria meningitidis
 (B) STRAIN: MCH88

20 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 116..643

25 (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 116..172

30 (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 173..643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

35 GTATCTTGAG GCATTGAAAA TATTACAATG CAAAAAGAAA ATTTTCAGTAT AATACGGCAG 60
 GATTCTTTAA CGGATTCTTA ACCATTTTTC TCCCTGACCA TAAAGGAATC AAGAT ATG 118
 Met
 -19

40 AAA AAA GCA CTT GCC GCA CTG ATT GCC CTC GCC CTC CCG GCC GCC GCA 166
 Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala Ala
 -15 -10 -5

45 CTG GCG GAA GGC GCA TCC GGC TTT TAC GTC CAA GCC GAT GCC GCA CAC 214
 Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala His
 1 5 10

50 GCC AAA GCC TCA AGC TCT TTA GGT TCT GCC AAA GGC TTC AGC CCG CGC 262
 Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro Arg
 15 20 25 30

55 ATC TCC GCA GGC TAC CGC ATC AAC GAC CTC CGC TTC GCC GTC GAT TAC 310
 Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp Tyr
 35 40 45

ACG CGC TAC AAA AAC TAT AAA CAA GTC CCA TCC ACC GAT TTC AAA CTT 358
 Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys Leu
 50 55 60

60 TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC TTC GAC ACC CAA TCC CCC 406
 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
 65 70 75

5 GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC CTC AAC CGC GCC TCC GTC 454
 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
 80 85 90

10 GAC TTT AAC GGC AGC GAC AGC TTC AGC CAA ACC TCC ACC GGC CTC GGC 502
 Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu Gly
 95 100 105 110

15 GTA TTG GCG GGC GTA AGC TAT GCC GTT ACC CCG AAT GTC GAT TTG GAT 550
 Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
 115 120 125

20 GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA GTC AAC ACT GTC AAA AAT 598
 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
 130 135 140

25 GTC CGT TCC GGC GAA CTG TCC GCC GGC GTA CGC GTC AAA TTC TGATATACGC 650
 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe
 145 150 155

GTTATTCCGC AAACCGCCGA GCCTTTCGGC GGTTTTGTTC TCCGCCGCCG CAACTACACA 710

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala
 -19 -15 -10 -5

40 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
 1 5 10

His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
 15 20 25

45 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
 30 35 40 45

50 Tyr Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys
 50 55 60

Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser
 65 70 75

55 Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser
 80 85 90

Val Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu
 95 100 105

60 Gly Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu
 110 115 120 125

Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys
 130 135 140
 5 Asn Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe
 145 150 155

(2) INFORMATION FOR SEQ ID NO:5:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 850 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: 24063
- 25 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 208..732
- 30 (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 208..264
- 35 (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 265..732
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
- 40 CACCCATCCG CCGCGTGATG CCGCCACCAC CATTAAAGG CAACGCGCGG GTTAACGGCT 60
 TTGCCGTCCG CAAAGCAGCC GGATACCGCT ACGTATCTTG AAGTATTAAA AATATTACGA 120
 45 TGCAAAAAGA AAATTTAAGT ATAATAAAGC AGAATTCTTT AACGGATTCT TAACAATTTT 180
 TCTAACTGAC CATAAAGGAA CCAAAT ATG AAA AAA GCA CTT GCC ACA CTG 231
 Met Lys Lys Ala Leu Ala Thr Leu
 -19 -15
- 50 ATT GCC CTC GCT CTC CCG GCC GCC GCA CTG GCG GAA GGC GCA TCC GGC 279
 Ile Ala Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly
 -10 -5 1 5
- 55 TTT TAC GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA 327
 Phe Tyr Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu
 10 15 20
- 60 GGT TCT GCC AAA GGC TTC AGC CCG CGC ATC TCC GCA GGC TAC CGC ATC 375
 Gly Ser Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile
 25 30 35

AAC GAC CTC CGC TTC GCC GTC GAT TAC ACG CGC TAC AAA AAC TAT AAA 423
 Asn Asp Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys
 40 45 50
 5 GCC CCA TCC ACC GAT TTC AAA CTT TAC AGC ATC GGC GCG TCC GCC ATT 471
 Ala Pro Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile
 55 60 65
 10 TAC GAC TTC GAC ACC CAA TCG CCC GTC AAA CCG TAT CTC GGC GCG CGC 519
 Tyr Asp Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg
 70 75 80 85
 15 TTG AGC CTC AAC CGC GCC TCC GTC GAC TTG GGC GGC AGC GAC AGC TTC 567
 Leu Ser Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe
 90 95 100
 AGC CAA ACC TCC ACC GGC CTC GGC GTA TTG GCG GGC GTA AGC TAT GCC 615
 Ser Gln Thr Ser Thr Gly Leu Gly Val Leu Ala Gly Val Ser Tyr Ala
 105 110 115
 20 GTT ACC CCG AAT GTC GAT TTG GAT GCC GGC TAC CGC TAC AAC TAC ATC 663
 Val Thr Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile
 120 125 130
 25 GGC AAA GTC AAC ACT GTC AAA AAC GTC CGT TCC GGC GAA CTG TCC GCC 711
 Gly Lys Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Ala
 135 140 145
 30 GGT GTG CGC GTC AAA TTC TGATATGCGC CTTATTCTGC AAACCGCCGA 759
 Gly Val Arg Val Lys Phe
 150 155
 GCCTTCGGCG GTTTTGTTTT CTGCCACCGC AACTACACAA GCCGGCGGTT TTGTACGATA 819
 35 ATCCCGAATG CTGCGGCTTC TGCCGCCCTA T 850

(2) INFORMATION FOR SEQ ID NO:6:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
 50 Met Lys Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala
 -19 -15 -10 -5
 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
 1 5 10
 55 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
 15 20 25
 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
 30 35 40 45
 60 Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu
 50 55 60

Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
 65 70 75
 5 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
 80 85 90
 Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu Gly
 95 100 105
 10 Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
 110 115 120 125
 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
 130 135 140
 15 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe
 145 150 155

20 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: b2

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 241..765

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 241..297

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 298..765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCC GCCTTT GCGGTTTTT CCAAACCGTT TGCAAGTTTC ACCCATCCGC CGCGTGATGC 60
 55 CGCCGTTTAA GGGCAACGCG CGGGTTAACG GATTGCGCGT CGGCAAAGCA GCCGGATGCC 120
 GCCGCGTATC TTGAGGCATT GAAATATTA CGATGCAAAA AGAAAATTTT AGTATAATAC 180
 60 GGCAGGATTC TTTAACGGAT TATTAACAAT TTTTCTCCCT GACCATAAAG GAACCAAAAT 240
 ATG AAA AAA GCA CTT GCC GCA CTG ATT GCC CTC GCA CTC CCG GCC GCC 288
 Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala
 -19 -15 -10 -5

GCA CTG GCG GAA GGC GCA TCC GGC TTT TAC GTC CAA GCC GAT GCC GCA 336
 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
 1 5 10
 5 CAC GCC AAA GCC TCA AGC TCT TTA GGT TCT GCC AAA GGC TTC AGC CCG 384
 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
 15 20 25
 10 CGC ATC TCC GCA GGC TAC CGC ATC AAC GAC CTC CGC TTC GCC GTC GAT 432
 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
 30 35 40 45
 15 TAC ACG CGC TAC AAA AAC TAT AAA GCC CCA TCC ACC GAT TTC AAA CTT 480
 Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu
 50 55 60
 20 TAC AGC ATC GGC GCG TCC GTC ATT TAC GAC TTC GAC ACC CAA TCG CCC 528
 Tyr Ser Ile Gly Ala Ser Val Ile Tyr Asp Phe Asp Thr Gln Ser Pro
 65 70 75
 25 GTC AAA CCG TAT TTC GGC GCG CGC TTG AGC CTC AAC CGC GCT TCC GCC 576
 Val Lys Pro Tyr Phe Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Ala
 80 85 90
 CAC TTG GGC GGC AGC GAC AGC TTC AGC AAA ACC TCC GCC GGC CTC GGC 624
 His Leu Gly Gly Ser Asp Ser Phe Ser Lys Thr Ser Ala Gly Leu Gly
 95 100 105
 30 GTA TTG GCG GGC GTA AGC TAT GCC GTT ACC CCG AAT GTC GAT TTG GAT 672
 Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
 110 115 120 125
 35 GCC GGC TAC CGC TAC AAC TAC GTC GGC AAA GTC AAC ACT GTC AAA AAC 720
 Ala Gly Tyr Arg Tyr Asn Tyr Val Gly Lys Val Asn Thr Val Lys Asn
 130 135 140
 GTC CGT TCC GGC GAA CTG TCC GCC GGC GTG CGC GTC AAA TTC TGATATACGC 772
 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe
 145 150 155
 GTTATTCGCG AAACCGCCGA GCCTTCGGCG GTTTTTCG 810

45 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

55 Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala
 -19 -15 -10 -5
 60 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
 1 5 10
 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
 15 20 25

Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
 30 35 40 45
 5 Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu
 50 55 60
 Tyr Ser Ile Gly Ala Ser Val Ile Tyr Asp Phe Asp Thr Gln Ser Pro
 65 70 75
 10 Val Lys Pro Tyr Phe Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Ala
 80 85 90
 His Leu Gly Gly Ser Asp Ser Phe Ser Lys Thr Ser Ala Gly Leu Gly
 95 100 105
 15 Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
 110 115 120 125
 20 Ala Gly Tyr Arg Tyr Asn Tyr Val Gly Lys Val Asn Thr Val Lys Asn
 130 135 140
 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe
 145 150 155
 25

(2) INFORMATION FOR SEQ ID NO:9:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: protein
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Neisseria meningitidis
 (B) STRAIN: 608B

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

45 Met Lys Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:10:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: protein
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Neisseria meningitidis
 (B) STRAIN: 608B
 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5 Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly Phe
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

15 (A) ORGANISM: Neisseria meningitidis
 (B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

20 Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala His Ala Lys
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: Neisseria meningitidis
 (B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

40 Ala Ala His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: Neisseria meningitidis
 (B) STRAIN: 608B

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Ser Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
 (B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp Tyr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
 (B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
 (B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
(B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
(B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
(B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val Asp Leu Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:20:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: 608B
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Ile
1 5 10 15

20 (2) INFORMATION FOR SEQ ID NO:21:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: 608B
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
Ser Gln Thr Ser Ile Gly Leu Gly Val Leu Thr Gly Val Ser Tyr
1 5 10 15

40 (2) INFORMATION FOR SEQ ID NO:22:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: 608B
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
Thr Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
(B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
(B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Tyr Ile Gly Lys Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
(B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Val Arg Ser Gly Glu Leu Ser Val Gly Val Arg Val Lys Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: 608B

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

20

Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr
1 5 10 15
Asp Phe Lys Leu Tyr Ser Ile Gly Ala
20 25